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ANALYSIS OF THE BIOLOGICAL DIVERSITY OF THE SKIN AND OROPHARYNGEAL MICROBIOTA DEPENDING ON VARIOUS TREATMENT METHODS FOR PSORIASIS

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АНАЛИЗ БИОЛОГИЧЕСКОГО РАЗНООБРАЗИЯ КОЖНОЙ И ОРОФАРИНГЕАЛЬНОЙ МИКРОБИОТЫ ПРИ РАЗЛИЧНЫХ МЕТОДАХ ТЕРАПИИ ПСОРИАЗА

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Abstract

Introduction. Psoriasis is a chronic inflammatory systemic disorder of a multifactorial origin, characterized by accelerated keratinocyte proliferation and impaired differentiation. Recently, the potential role of the human microbiota in the emergence of various chronic conditions, including psoriasis, has become a popular area of research. At the same time, no specific microbiological markers have been identified that could be used to accurately evaluate treatment effectiveness. The aim of the study was to assess the biological diversity of microbial communities of the skin and oropharynx in patients receiving different psoriasis treatment regimens, and to investigate an association between the incidence of isolated individual microorganisms and the applied treatment method.

Materials and methods. The study included 155 male and female patients, aged >18 years old, with psoriasis vulgaris of varying severity. All patients were divided into three groups. Group 1 – patients receiving topical corticosteroids (N=52); group 2 – patients receiving methotrexate (N=51); Group 3 – patients receiving IL-17 inhibitors (N=52). Microbiological examination of skin and oropharynx swabs was conducted for all patients. The identification of microorganisms was performed using MALDI-ToF mass spectrometry.

Results. In general, 109 and 139 individual species were isolated from oropharynx and skin, respectively. Analyzing biological diversity of the oropharyngeal microbiota revealed that the following microbial species are referred to resident microbiota in patients from all three groups: *Streptococcus salivarius, Neisseria subflava, Streptococcus vestibularis*. Differences in the microbiological diversity between the studied groups were only revealed due to an additional oropharyngeal microbiota. Analysis of the microbial diversity of the skin microbiota showed, that none of the isolated microorganisms was a resident part of the microbiota in all patients. Statistically significant differences were obtained for skin microorganisms, such as *Staphylococcus hominis* (p = 0.047) and *Enterococcus*

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faecalis (p = 0.013), as well as oropharyngeal microorganisms, including *Neisseria flavescens* (p = 0.022), *Micrococcus luteus* (p = 0.048) and *Acinetobacter ursingii* (p = 0.040).

Conclusion. Thus, there has been revealed significant differences between studied groups in isolating individual microorganisms, which may potentially show varying effectiveness for different approaches to manage psoriatic patients.

Keywords: skin microbiota, oropharyngeal microbiota, psoriasis, biological diversity, psoriasis treatment, IL-17 inhibitors, methotrexate.

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Резюме

Введение. Псориаз – хроническое воспалительное системное заболевание мультифакториальной природы, характеризующееся ускоренной пролиферацией кератиноцитов и нарушением их дифференцировки. В настоящее время популярной темой для исследований становится влияние человеческого микробиома на развитие различных хронических заболеваний, в том числе псориаза. При этом, до сих пор не найдены конкретные микробиологические маркеры, которые позволяли бы оценивать эффективность его лечения. Цель исследования - оценить биологическое разнообразие микробных сообществ кожи и ротоглотки пациентов, получающих различные виды лечения псориаза, а также изучить связи между частотой выделения отдельных микроорганизмов и применяемым методом лечения.

Материалы и методы. В исследование были включены 155 пациентов мужского и женского пола возрастом старше 18 лет с вульгарным псориазом различной степени тяжести. Все пациенты были распределены по трем группам. Группа 1 включала пациентов, получающих топические глюкокортикостероиды (n=52); группа 2 – пациентов, получающих метотрексат (n=51); группа 3 – пациентов, получающих терапию в виде ингибиторов IL-17 (n=52). Всем пациентам было проведено микробиологическое исследование мазков кожи и ротоглотки. Идентификация микроорганизмов проводилась с помощью метода MALDI-ToF масс-спектрометрии. **Результаты.** В общей сложности из ротоглотки было выделено 109 видов микроорганизмов, с кожных покровов – 139 видов. Анализ биологического разнообразия орофарингеальной микробиоты показал, что к группе постоянной микробиоты пациентов всех трех групп относятся следующие виды микроорганизмов: *Streptococcus salivarius, Neisseria subflava, Streptococcus vestibularis*. Различия между группами были выявлены только за

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счет добавочной микробиоты. В ходе анализа биологического разнообразия микробиоты кожных покровов было выявлено, что ни один из выделенных микроорганизмов не является постоянным компонентом микробиоты во всех исследуемых группах пациентов с псориазом. Были получены статистически значимые различия для кожных микроорганизмов, таких как *S. hominis* (p = 0,047) и *E. faecalis* (p = 0,013), а также для орофарингеальных микроорганизмов: *N. flavescens* (p = 0,022), *M. luteus* (p = 0,048), *Acinetobacter ursingii* (p = 0,040).

Выводы. Таким образом, в ходе нашего исследования были выявлены значимые отличия между данными группами по частоте выделения отдельных микроорганизмов, что потенциально может отражать различия в успешности отдельных подходов к ведению пациентов с псориазом.

Ключевые слова: кожная микробиота, микробиота ротоглотки, псориаз, биологическое разнообразие, лечение псориаза, ингибиторы IL-17, метотрексат.

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1 Inroduction

Psoriasis is a chronic inflammatory systemic disorder of a multifactorial origin, characterized by accelerated proliferation and impaired differentiation of keratinocytes. Several factors contribute to the development of this disease, including hereditary predisposition, abnormalities in the immune, endocrine and nervous systems, as well as various types of adverse external influences (stress, infection, smoking, etc.). Psoriasis is often linked with other general medical conditions, which makes it not only a serious dermatological disease, but also cause its' significant impact on the overall human health [4, 9, 10].

The treatment of patients with psoriasis involves several approaches. The recommended first-line treatment includes topical corticosteroids. In moderate to severe cases of the disease, systemic treatment is prescribed. The most common drug in this case is the cytostatic agent methotrexate. Recently, biological therapy with such remedies as tumor necrosis factor-α (TNF-α) inhibitors, interleukin-23 (IL-23) inhibitors and interleukin-17 (IL-17) inhibitors has also become widespread [7].

So far, the potential role of the human microbiota in the emergence of various chronic conditions, including psoriasis, has become a popular area of research. Studies have shown that the microbiota in various loci plays an important role in the immune system functioning and inflammation regulation, which makes microbes a key factor in the emergence of psoriasis-related pathological processes. Individual studies have shown that there are certain correlations between the microbiological communities composition and the psoriasis severity [8].

According to results of different researches of the skin microbiota, patients with psoriasis were significantly more likely to have certain bacterial taxa, such as *Streptococcus* spp. and *Staphylococcus* spp., compared to healthy people. They were also less likely to have other taxa, such as *Cutibacterium* spp. and *Malassezia* spp [8]. In another study, the researchers also found a lower incidence of *Cutibacterium* spp. in patients with psoriasis, which are described as short-chain fatty acids

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producing commensals, and a higher incidence of the *Streptococcus* spp., which has been associated with an exacerbations of the disease [13].

There are also certain differences in the composition of the oropharyngeal microbiota between patients with psoriasis and healthy individuals. In one study, Zhao et al. (2024) used saliva samples from patients from control and experimental groups as biological material. Using 16S rRNA sequencing, the researchers found that the diversity of the microbiota in patients with psoriasis was greater than in the control group mainly due to the presence of *Porphyromonas* spp., *Neisseria* spp., *Haemophilus* spp., *Alloprevotella* spp. and *Prevotella* spp. Additionally, a positive correlation was found between the severity of psoriasis and some of these bacterial taxa (*Porphyromonas* spp., *Neisseria* spp., *Alloprevotella* spp.) [15]. In a similar study a connection was found between psoriasis and the oropharyngeal microbiota as well as levels of inflammatory proteins in saliva [2].

During the study of the microbiota in the palatine tonsils of patients with psoriasis, a resident pathogenic microbiota (*Staphylococcus aureus, Staphylococcus haemolyticus* and *Streptococcus pyogenes*) was often found in most of the studied cases. This, in turn, may suggest a possible link between psoriasis and chronic tonsillitis. At the same time, an increased immunological reactivity of the palatine tonsils to streptococcal infection can lead to an increase in the number of activated T-cells, which enhance the inflammatory response, which, in turn, could worsen skin lesions in patients [1].

At the same time, despite extensive research of the biological diversity of the skin and oral microbiota in psoriasis patients, no specific microbiological markers have been identified that could be used to accurately evaluate the effectiveness of treatment. In addition, most studies on the relationship between microorganisms and this disease focus on intestinal communities, while skin and, in particular, oropharyngeal microbiota are often overlooked.

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The aim of the study was to assess the overall biological diversity of microbial communities of the skin and oropharynx of patients receiving different types of psoriasis treatment, as well as to investigate the association between the isolation frequency of individual skin and oropharyngeal microorganisms and the applied treatment method.

2 Materials and Methods

The study included male and female 155 patients, aged from 18 years old, with psoriasis vulgaris of varying severity. All patients were divided into three groups. The group 1 consisted of patients who received different topical corticosteroids (N=52), the group 2 consisted of patients who received methotrexate (N=51), and the group 3 consisted of patients who received different IL-17 inhibitors (N=52).

The treatment of patients in the studied groups lasted from 6 months to 3 years. The exclusion criteria for the study included the presence of alcohol and drug addiction in patients, pregnancy and concomitant pathologies that significantly affect life expectancy (severe liver and kidney failure, severe chronic lung diseases, oncological diseases, acute cardiovascular pathology, heart failure, stroke or transient ischemic attack in the anamnesis).

The study was approved by Protocol № 287 of the Bioethics Committee of Samara State Medical University. Voluntary informed consent was obtained from all patients included in the study.

Microbiological examination of skin (from the areas of specific lesions) and oropharynx swabs was conducted in all patients. Inoculation was carried out on universal chromogenic agar (HiMedia, India) and Muller-Hinton agar supplemented with 5% sheep blood (HiMedia, India), under microaerobic conditions (5% atmospheric CO_2 content) for incubation. Also, using the Bactron 300-2 anaerobic chamber (Sheldon Manufacturing, USA), the material was inoculated and incubated

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under anaerobic conditions using universal chromogenic agar, Muller-Hinton agar with the addition of 5% sheep blood and anaerobic agar (HiMedia, India). In addition, Saburo agar with chloramphenicol (HiMedia, India) was used for inoculation and incubation under aerobic conditions and for the isolation of fungi. Incubation of material were carried out for 24 hours under microaerobic conditions and for 72 hours under anaerobic conditions at 37 °C. Incubation of material on Saburo agar was carried out for one week at 28 °C. The identification of microorganisms was performed using the MALDI-ToF mass spectrometry technique on a Microflex LT (Bruker Daltonics GmbH, Germany) via direct application method.

The coefficient of constancy (C) was calculated to analyze microbial diversity at the studied loci. In the case of isolation of individual microorganisms from more than 50% of patients, this microorganism was regarded as part of the resident microbiota. The isolation from patients in the range of 25–50% corresponded to an additional microbiota, isolation less than in 25% of cases corresponded to transient microbiota. Coefficient was calculated using the following formula: $C=(p \times 100)/P$, in which p - number of isolations of individual microorganisms, P - total number of patients.

Statistical analysis was carried out using the Stat Tech v. 4.6.1. program (Stattech LLC, Russia). Categorical data was presented in terms of absolute values and percentages. The percentages were compared using the Pearson's Chi-square test in the analysis of the multipole conjugacy tables. A posteriori comparisons were conducted using the Pearson's chi-squared test with the Holm correction. The differences were found to be statistically significant at the $p\text{-value} < 0.05$.

3 Results

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The total number of individual microorganisms isolated from studied patients was 183. 109 species were isolated from the oropharynx and 139 species were isolated from the skin.

An analysis of the oropharyngeal microbiota diversity in patients treated with topical corticosteroids showed that the resident microbiota of the locus consists of three main types of microorganisms: *Streptococcus salivarius* (present in 90.2% of samples), *Neisseria subflava* (74.5%) and *Streptococcus vestibularis* (56.9%). Additional microbiota in patients of the group 1 consisted of 7 species of microorganisms: *Streptococcus parasanguinis* (39,2%), *Rothia dentocariosa* (39,2%), *Neisseria flavescens* (37,3%), *Rothia mucilaginosa* (35,3%), *Staphylococcus aureus* (33,3%), *Streptococcus oralis* (31,4%), *Streptococcus mitis* (27,5%).

Three species of microorganisms have been assigned to resident oropharyngeal microbiota in patients treated with methotrexate: *S. salivarius* (78,4%), *N. subflava* (66,7%), *S. vestibularis* (52,9%). Five species were assigned to additional microbiota: *S. mitis* (33,3%), *S. parasanguinis* (31,4%), *S. oralis* (31,4%), *N. flavescens* (29,4%), *R. mucilaginosa* (25,5%).

In patients treated with IL-17 inhibitors, the following species were assigned to the resident oropharyngeal microbiota: *S. salivarius* (79,2%), *N. subflava* (67,9%), *S. vestibularis* (58,5%). Among the additional microbiota, 4 species of microorganisms were identified, including: *R. mucilaginosa* (43,4%), *R. dentocariosa* (34,0%), *S. aureus* (32,1%), *S. parasanguinis* (28,3%).

Distribution of representatives of resident and additional oropharyngeal microbiota is demonstrated in Figure 1.

In addition, the following genera of the transitional oropharyngeal microbiota were isolated from patients of the studied groups: *Acinetobacter (A. baumanii, A. calcoaceticus, A. johnsonii, A. junii, A. lactucae, A. lwoffii, A. pittii, A. ursingii),*

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Actinomyces (A. naeslundii, A. oris,), Candida (C. albicans, C. dubliniensis, C. glabrata, C. parapsilosis, C. tropicalis), Citrobacter (C, freundii, C. koseri), Corynebacterium (C. amycolatum, C. argentoratense, C. durum, C. sanguinis), Enterobacter (E. asburiae, E. bugandensis, E. cloacae), Enterococcus (E. durans, E. faecalis), Granulicatella (G. adiacens, G. elegans), Haemophilus (H. parahaemolyticus, H. parainfluenzae), Klebsiella (K. oxytoca, K. pneumoniae), Lactobacillus (L. fermentum, L. plantarum), Lacticaseibacillus (L. paracasei, L. rhamnosus, L. sharpeae), Micrococcus (M. lylae, M. luteus), Neisseria (N. cinerea, N. elongata, N. macacae, N. mucosa, N. oralis, N. perflava, N. polysaccharea), Pseudomonas (P. aeruginosa, P. japonica, P. stutzeri), Rothia (R. aeria, R. kristinae), Staphylococcus (S. borealis, S. capitis, S. epidermidis, S. haemolyticus, S. hominis, S. lugdunensis, S. pasteuri, S. warneri), Streptococcus (S. agalactiae, S. anginosus, S. australis, S. constellatus, S. gordonii, S. infantis, S. mutans, S. peroris, S. pneumoniae, S. pseudopneumoniae, S. sanguinis, S. sobrinus), Veillonella (V. atypica, V. dispar, V. parvula, V. rogosae).

Also in individual cases following oropharyngeal microorganisms were isolated: representatives of *Enterobacterales* (*Escherichia coli, Morganella morganii, Pichia fermentans, raoultella ornithinolytica, Serratia marcescens), Aeromonas hydrophila, aggregatibacter aphrophilus, Aspergillus niger, tructae Chryseobacterium, Fusobacterium canifelinum, haemolysans Gemella, Kluyveromyces marxianus, kocuria rhizophila, Lactococcus garvieae, Lautropia mirabilis, Ligilactobacillus salivarius, Limosilactobacillus fermentum, Meyerozyma guilliermondii, Moraxella osloensis, Peribacillus simplex, Rhodotorula mucilaginosa*.

Therefore, differences in the microbiological diversity between the studied groups were only revealed due to an additional part of oropharyngeal microbiota.

During the analysis of the microbial diversity of the skin microbiota, it was found that none of the isolated microorganisms was a resident part of the microbiota

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in all studied groups. At the same time, four species of microorganisms were identified as additional microbiota in group 1: *Staphylococcus epidermidis* (43,1%), *Micrococcus luteus* (37,3%), *Staphylococcus capitis* (31,4%), *Staphylococcus hominis* (25,5%). In patients of the group 2, 3 species of microorganisms were identified as additional microbiota: *S. epidermidis* (43,1%), *S. hominis* (33,3%), *M. luteus* (25,5%). In patients from group 3, four species were distinguished: *S. epidermidis* (49,1%), *S. hominis* (49,1%), *M. luteus* (41,5%), *S. aureus* (26,4%).

Distribution of representatives of additional skin microbiota is demonstrated in Figure 2.

The following genera of transient skin microbiota were also isolated from patients of the studied groups: *Acinetobacter (A. baumanii, A. johnsonii, A. junii, A. lactucae, A. lwoffii, A. parvus, A. pittii, A. radioresistens, A. schindleri, A. ursingii, A. variabilis), Actinomyces (A. oris, A. timonensis), Bacillus (B. amyloliquefaciens, B. cereus, B. megaterium, B. pumilus, B. subtilis), Brachybacterium (B. conglomeratum, B. muris), Brevibacterium (B. casei, B. luteolum), Corynebacterium (C. accolens, C. afermentans, C. amycolatum, C. aurimucosum, C. coyleae, C. freneyi, C. jeikeium, C. minutissimum, C. mucifaciens, C. sanguinis, C. simulans, C. striatum, C. tuberculostearicum, C. xerosis), Enterococcus (E. faecalis, E. faecium), Janibacter (J. indicus, J. hoylei), Klebsiella (K. aerogenes, K. oxytoca, K. pneumoniae), Kocuria (K. marina, K. palustris, K. rhizophila), Neisseria (N. elongata, N. flavescens, N. subflava, N. macacae, N. mucosa), Pantoea (P. agglomerans, P. dispersa, P. septica), Pseudomonas (P. luteola, P. monteilii, P. oryzihabitans, P. stutzeri), Rothia (R. amarae, R. dentocariosa, R. kristinae, R. mucilaginosa, R. terrae), Staphylococcus (S. auricularis, S. borealis, S. caprae, S. cohnii, S. haemolyticus, S. lugdunensis, S. nepalensis, S. pasteuri, S. petrasii, S. pettenkoferi, S. piscifermentans S. saprophyticus, S. warneri), Streptococcus (S. agalactiae, S. anginosus, S. gordonii, S. infantis, S. mitis, S. mutans, S. oralis, S.*

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parasanguinis, S. salivarius, S. sanguinis, S. urinalis, S. vestibularis), Streptomyces (S. albogriseolus, S. tanashiensis)

Additionally, in individual cases following skin microorganisms were isolated: *Aerococcus viridans, Alternaria alternata, Aspergillus niger, Brevundimonas diminuta, Candida parapsilosis, Chryseobacterium hominis, Cutibacterium avidum, Deinococcus wulumuqiensis, Dermabacter hominis, Enterobacter cloacae, Granulicatella adiacens, Gordonia rubripertincta, Helcobacillus massiliensis, Kytococcus schroeteri, Lactobacillus fermentum, Lactococcus garvieae, Limosilactobacillus fermentum, Lysinibacillus fusiformis, Microbacterium paraoxydans, Micrococcus lylae, Moraxella osloensis, Paenibacillus lautus, Penicillium chrysogenum, Peribacillus simplex, Pseudarthrobacter oxydans, Raoultella ornithinolytica, Rhodotorula mucilaginosa, Sphingobacterium hotanense, Turicella otitidis, Veillonella dispar, Winkia neuii.*

The frequency of microbial isolation from the skin and oropharyngeal loci was analyzed in relation to the study group (using the Pearson chi-squared test) (Table 1). Statistically significant differences were observed for skin microorganisms, such as *Staphylococcus hominis* ($p = 0.047$) and *Enterococcus faecalis* ($p = 0.013$), as well as oropharyngeal microorganisms, including *Neisseria flavescens* ($p = 0.022$), *Micrococcus luteus* ($p = 0.048$) and *Acinetobacter ursingii* ($p = 0.040$). In group 1, *N. flavescens* was the most commonly detected species (36.5%). In contrast, in group 3, it was detected less frequently, with only 13.2% of samples containing this microbe. In group 1, *M. luteus* was also the most frequently isolated microorganism (5.8%) and *A. ursingii* was more frequently isolated in group 2 (6.0%). Among the skin microorganisms identified during the study, *S. hominis* was the most prevalent in group 3 (accounting for 49.1% of the cases), while *E. faecalis* was predominant in group 2 (accounting for 8.0%).

4 Discussion

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At present, the specific details of individual psoriasis treatment methods are most extensively explored in the context of the intestinal microbiota, as it was previously mentioned. For example, Yeh et al. in 2019, demonstrated that immunological, cytostatic and biological methods of psoriasis treatment can lead to changes in the composition of microbiological communities in the gastrointestinal tract. This, in turn, results in alterations in intestinal metabolism and the regulation of immune responses in host cells [14].

At the same time, research of skin and oropharyngeal communities, aimed not only at general biological diversity but rather at the species composition in relation to various psoriasis treatment methods, is practically non-existent.

When analyzing the diversity of cutaneous and oral microbiota in patients with psoriasis, we found a generally homogenous structure of microbial communities in all studied groups. Therefore, the normal microbiota of the mucosal membranes of the oropharynx is dominated by *Streptococcus* spp., *Neisseria* spp. and *Rothia* spp., while the cutaneous microbiota is primarily composed of coagulase-negative representatives of the *Staphylococcus* spp. Interestingly, in patients of the group 3, the additional skin microbiota, as well as the additional oropharyngeal microbiota in patients of group 1 and group 3, also included *S. aureus*, although there were no significant differences between the groups in the isolation frequency of this microorganism.

As previously mentioned, the oropharynx has a high diversity of microorganisms, that can be involved in immunopathological processes, and plays a significant role in the development of various systemic illnesses. However, at present, there is a lack of sufficient data regarding the association between alterations in the species composition of oropharyngeal microbiota and the development of psoriasis and the treatment methods used. However, our study has revealed a certain correlation between the incidence of individual microorganisms and the method of psoriasis treatment.

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The most interesting finding was for the representative of the additional oropharyngeal microbiota *N. flavescens,* for which significant differences were found between the studied groups. Although there is a lack of data in the scientific literature on the potential involvement of this specific microorganism in the pathogenesis of psoriasis, the above information has already indicated an increased frequency of bacterial isolates of this genus from psoriatic patients. There is also information regarding an increase in the incidence of *Neisseria* spp. in patients with active forms of autoimmune pathologies, such as celiac disease. In particular, some researchers have reported that *N. flavescens* may also be implicated in the pathological processes associated with this disease [3, 5]. Additionally, a case of infectious lesion of the lingual tonsils caused by *N. flavescens* has been reported [10]. All this information may suggest the possible involvement of this microorganism in inflammatory processes.

More specific information in this regard can be found for skin microbiota. In 2019 Langan et al. conducted a study on skin microorganisms with the aim of investigating the impact of various treatment modalities on the balance of *Actinobacteria* and *Firmicutes* in patients with psoriasis. As a result of the research, the scientists discovered that, compared to the microbiota found on the skin of healthy individuals, psoriasis is associated with an increase of *Firmicutes* and a corresponding reduction of *Actinobacteria*. It has been demonstrated that various treatment modalities restore this balance, with biological therapy demonstrating a particularly potent effect on it and yielding the most significant outcomes [6].

In our study, we also identified a particularly interesting pattern among patients receiving biological treatment. *S. hominis* was significantly more prevalent in group 3. This microorganism, similar to other coagulase-negative staphylococci, has the ability to inhibit the growth of pathogenic microorganisms, especially *S. aureus*, which is often involved in inflammatory processes of the skin associated with psoriasis. In particular, phenol-soluble modulins (PSMs) and lantibiotics

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produced by *S. hominis* have been shown to act as synergistic partners with the human antimicrobial peptide LL-37 in eliminating *S. aureus* [11]. Therefore, an increased representation of *S. hominis* within the skin microbiota may potentially serve as a marker for the effectiveness of therapy.

5 Conclusion

Although the studied groups of psoriatic patients undergoing different types of treatment exhibited a small amount of differences in general biological diversity of the skin and oropharyngeal microbiota , our research identified significant differences between these groups with regard to the isolation frequency for individual microorganisms, which may potentially indicate differences in the effectiveness of various treatment approaches for these patients. It would be rational to pursue similar research in the future to identify additional indicators of the efficacy of psoriasis management. The study also demonstrated the potential for using a culturomics-based approach to assess the biological diversity of the skin and oropharyngeal microbiota in patients with psoriasis.

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ТАБЛИЦЫ

Table 1. Analysis of isolation frequency of individual skin and oropharyngeal microorganisms depending on applied therapy.

Microorganism	Locus	Isolation frequency			p
		Group 1 abs, %	Group 2 abs, %	Group 3 abs, %	
Neisseria flavescens	Oropharynx	19 (36,5)	14 (28,0)	7 (13,2)	0,022 $p_{group\ 1\ –\ group\ 3}$ = 0,017
Micrococcus luteus	Oropharynx	3 (5,8)	0 (0,0)	0 (0,0)	0,048
Acinetobacter ursingii	Oropharynx	0 (0,0)	3 (6,0)	0 (0,0)	0,040
Staphylococcus hominis	Skin	14 (26,9)	16 (32,0)	26 (49,1)	0,047
Enterococcus faecalis	Skin	0 (0,0)	4 (8,0)	0 (0,0)	0,013

Notes: the statistical method applied is Pearson chi–square test (differences between groups were statistically significant at $p < 0.05$).

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РИСУНКИ

Figure 1. Species diversity of resident and additional oropharyngeal microbiota in psoriatic patients depending on applied therapy.

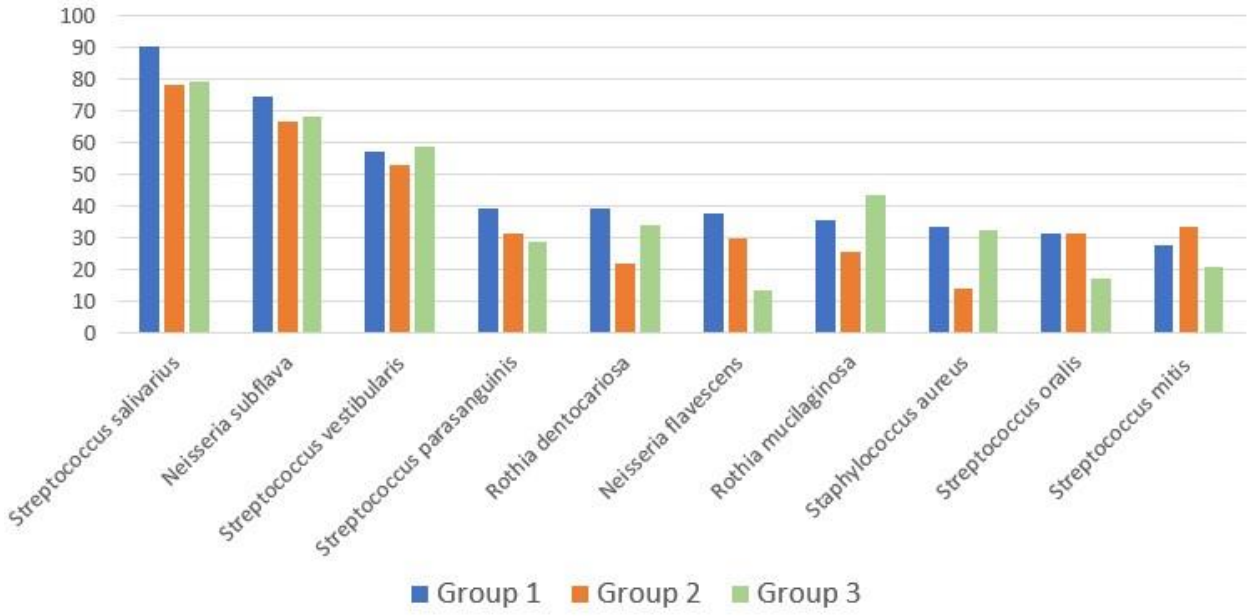

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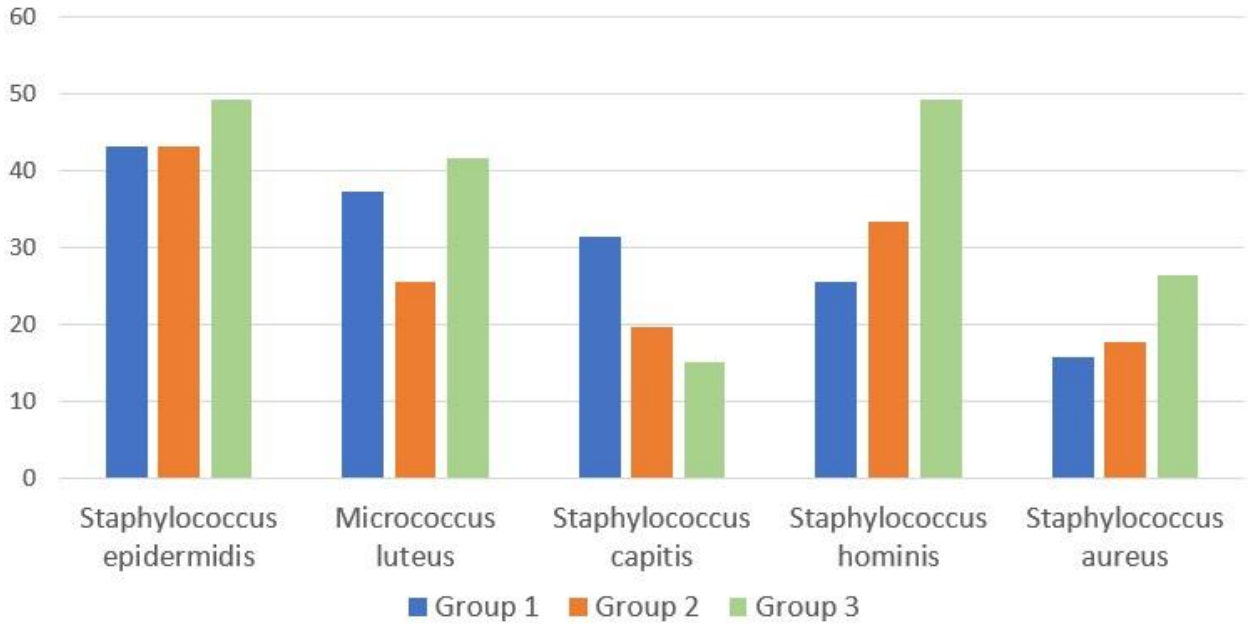
Figure 2. Species diversity of additional skin microbiota in psoriatic patients depending on applied therapy.



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Блок 3. Метаданные статьи

ANALYSIS OF THE BIOLOGICAL DIVERSITY OF THE SKIN AND OROPHARYNGEAL MICROBIOTA DEPENDING ON VARIOUS TREATMENT METHODS FOR PSORIASIS

АНАЛИЗ БИОЛОГИЧЕСКОГО РАЗНООБРАЗИЯ КОЖНОЙ И ОРОФАРИНГЕАЛЬНОЙ МИКРОБИОТЫ ПРИ РАЗЛИЧНЫХ МЕТОДАХ ТЕРАПИИ ПСОРИАЗА

Сокращенное название статьи для верхнего колонтитула:

SKIN AND OROPHARYNX MICROBIOTA IN THE PSORIASIS TREATMENT

МИКРОБИОТА КОЖИ И РОТОГЛОТКИ ПРИ ЛЕЧЕНИИ ПСОРИАЗА

Keywords: skin microbiota, oropharyngeal microbiota, psoriasis, biological diversity, psoriasis treatment, IL-17 inhibitors, methotrexate.

Ключевые слова: кожная микробиота, микробиота ротоглотки, псориаз, биологическое разнообразие, лечение псориаза, ингибиторы IL-17, метотрексат.

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